

Syphilis and HIV co-infection in Thai medical school hospital

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Background: HIV and syphilis affect similar patient groups and co-infection is common. In HIV infected patients, clinical manifestation of syphilis may be atypical and different from HIV uninfected cases. This study aimed to compare the characteristics of syphilis between HIVseropositive and HIVseronegative patients in Thai Medical School Hospital.

Methods: Retrospectively chart review of new cases of syphilis who attended the STD clinic, Chulalongkorn Hospital, Bangkok, Thailand from 1st June 2001 to 31st May 2006 was conducted.

Results: There were totally 385 new cases of syphilis during the studied period and HIV screening was done in 325 patients. The prevalence of HIV infection among syphilis patients was 33.2%. We found that younger age, male gender, and men who have sex with men (MSM) were significantly associated with HIV infection ($p < 0.05$). Secondary syphilis was more common manifestation in HIV infected individuals ($p < 0.005$). Syphilis among HIV infected patients had significantly lower VDRL titer ($p < 0.005$) and 15.9% had nonreactive VDRL.

Conclusion: HIV co-infection should be considered in syphilitic clients particularly with younger age, being male gender, MSM, and whose clinical manifestations are secondary syphilis. Non-reactive or low titer VDRL does not exclude syphilis in HIV infected patients and treponemal antibody test is needed for screening and diagnosis.

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Genotyping of *Chlamydia trachomatis* and human papillomavirus in clinical specimens from North-Eastern CroatiaZ. Bosnjak¹, M. Peric¹, D. Pavlinic^{2,*}, S. Dzijan³, I. Roksandic-Krizan¹, D. Vukovic¹, N. Ruzman¹, J. Burazin¹, G. Lauc³, A. Antolovic-Pozgain¹¹ *INSTITUTE of Public Health for Osijek-Baranya County, Osijek, Croatia*² *School of Medicine, Osijek, Croatia*³ *School of Medicine, DNA Laboratory, Osijek, Croatia*

Background: Human papillomavirus (HPV) and *Chlamydia trachomatis* (Ct) are major causes of sexually transmitted diseases. Clinical consequences of high-risk HPV (HR HPV) infection, especially with HPV types HPV 16 and HPV 18, include abnormal Pap test results, low and high-grade cervical intraepithelial neoplasia and cervical cancer, for which Ct may sometimes be a cofactor. The aim of the study was to determine the prevalence of Ct and age-related profiles of HR HPV infections among cases of other sexually transmitted infections in our county.

Methods: Due to the chronic and "silent" infection of Ct, fast molecular diagnostics and adequate therapy of the infected individuals are the crucial steps in the Ct spread

HPV with normal and abnormal cervical cytological diagnosis. Subsequently all Ct positive samples were analysed by sequencing of the amplified *omp1* fragments using Applied Biosystem 3130 Genetic Analyser. Genotyping and sequence mutation analysis were performed using ABI SEQSCAPE software and compared with the reference sequences of all known Ct serotypes. HR HPV positive samples with abnormal cervical cytological diagnosis were genotyped by Linear Array HPV Genotyping Test (Roche Diagnostics).

Results: The determined serotype of Ct and HPV genotypes distribution were compared with the Ct and HPV distribution pattern in other regions of the world. The association between certain HPV genotype and cervical intraepithelial neoplasia was determined as well as mixed infections with four or more HPVs. The most prevalent Ct genotype in Osijek-Baranya County was serotype E (in concordance with Sweden and Taiwan data), followed by F, K, G, D, B and J (differs from Sweden and Taiwan data). The sequence of *omp1* gene showed limited variation. HPV 16 and HPV 18 were the most common HR HPV genotypes in the cervical specimens with abnormal cervical cytological diagnosis. Obtained results also determined mixed infection of four HR HPV with one or more low risk HPV.

Conclusion: The obtained results for Ct and HPV and further analyses in this ongoing project could be useful tool for clinical and epidemiological characterization of circulating pathogens in our community.

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Frequent infections in Mexican women experiencing spontaneous pregnancy lossL. Conde-Ferrández^{1,*}, R. Suarez-Allen¹, L. Manzano-Cabrera¹, M.R. Gonzalez-Losa¹, G. Koh-Tec², M. Perez-Tuyub², J. Camara-Mejia¹, J. Carrillo-Martinez³, M. Puerto-Solis¹¹ *Centro de Investigaciones Regionales, Universidad Autónoma de Yucatán, Mérida, Yucatán, México*² *Universidad Autónoma de Yucatán, Mérida, Yucatán, México*³ *Instituto Mexicano del Seguro Social, Mérida, México*

Background: Some maternal infections especially during the early gestation can result in fetal loss or malformations. Gestation represents an altered immunological state which could predispose to various infections, and in particular, latent viral infections might be reactivated during this period. In this study we aimed to determine the prevalences of viral and protozoan pathogens, within women at reproductive age experiencing spontaneous pregnancy loss in southeast Mexico, and the epidemiological variables present.

Methods: Women requiring medical attention for spontaneous abortion in a Social Security Hospital were randomly invited to participate. After consent, an interview was applied; serology tests for IgM antibodies against human cytomegalovirus (CMV), Herpes Simplex virus (HSV), and *Tox-*